



IFWO

## RAW SEQUENCE LISTING

DATE: 07/28/2004

PATENT APPLICATION: US/10/783,297A

TIME: 16:41:00

Input Set : A:\SEQ List.ST25amended2.txt

Output Set : N:\CRF4\07282004\J783297A.raw

3 <110> APPLICANT: Johnson & Johnson Pharmaceutical Research and development  
 5 <120> TITLE OF INVENTION: HUMAN CYCLOOXYGENASE-3 AND USES THEREOF  
 7 <130> FILE REFERENCE: PRD-2041  
 9 <140> CURRENT APPLICATION NUMBER: US/10/783,297A  
 10 <141> CURRENT FILING DATE: 2004-02-20  
 12 <160> NUMBER OF SEQ ID NOS: 15  
 14 <170> SOFTWARE: PatentIn version 3.2  
 16 <210> SEQ ID NO: 1  
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 18 <212> TYPE: DNA  
 19 <213> ORGANISM: Artificial Sequence  
 21 <220> FEATURE:  
 22 <223> OTHER INFORMATION: Primer/probe  
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 29 <211> LENGTH: 25  
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 34 <223> OTHER INFORMATION: Primer/probe  
 36 <400> SEQUENCE: 2  
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 42 <212> TYPE: DNA  
 43 <213> ORGANISM: Homo sapiens  
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 52 <211> LENGTH: 31  
 53 <212> TYPE: PRT  
 54 <213> ORGANISM: Homo sapiens  
 56 <400> SEQUENCE: 4  
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 59 1 5 10 15  
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 66 <210> SEQ ID NO: 5  
 67 <211> LENGTH: 93  
 68 <212> TYPE: DNA  
 69 <213> ORGANISM: Homo sapiens



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74 caggctcagc cctcatctc tctcctctgc agg                                     93
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78 <211> LENGTH: 31
79 <212> TYPE: PRT
80 <213> ORGANISM: Homo sapiens
82 <400> SEQUENCE: 6
84 Glu Cys Asp Pro Gly Ala Arg Trp Gly Ile Phe Leu Ala Ser Gly Gly
85 1          5          10          15
88 Ala Leu Asn Ala Arg Leu Ser Pro Ser Leu Ser Ser Ala Gly
89          20          25          30
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93 <211> LENGTH: 24
94 <212> TYPE: DNA
95 <213> ORGANISM: Artificial Sequence
97 <220> FEATURE:
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105 <211> LENGTH: 1893
106 <212> TYPE: DNA
107 <213> ORGANISM: Homo sapiens
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116 acgccagtga atccctgttg ttactatcca tgccagcacc agggcatctg tgtccgcttc      240
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120 atccctggcc tgtggacctg gctccggaat tcactgcggc ccagccctc tttcaccac      360
122 ttctgtctca ctacggggcg ctggttctgg gagtttgtca atgccacctt catccgagag      420
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126 aactcagcac atgactacat cagctgggag tctttctcca acgtgagcta ttacactcgt      540
128 attctgcccct ctgtgcctaa agattgcccc acacccatgg gaaccaaagg gaagaagcag      600
130 ttgccagatg cccagctcct ggcccgcgcg ttcctgtctc ggaggaagtt catacctgac      660
132 cccaaggcca ccaacctcat gtttgcttcc tttgcacaac acttcaccca ccagttcttc      720
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138 aaactcaagt accaggtgct ggatggagaa atgtacccgc cctcggtaga agaggcgctt      900
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142 gtgtttgggc tgcttctctg gctcatgctg tatgccacgc tctggctacg tgagcacaac     1020
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146 acgacccgcc tcactctcat aggggagacc atcaagattg tcatcgagga gtacgtgcag      1140
148 cagctgagtg gctatttctt gcagctgaaa tttgaccagc agctgctgtt cgggtgccag      1200
150 ttccaatacc gcaaccgcat tgccatggag ttcaaccatc tctaccactg gcacccctc      1260
152 atgcctgact ctttcaagggt gggctcccag gagtacagct acgagcagtt cttgttcaac      1320
154 acctccatgt tgggtggacta tggggttgag gccctgggtg atgccttctc tcgcagatt      1380
156 gctggccgga tcggtggggg caggaacatg gaccaccaca tcctgcatgt ggctgtggat      1440

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158 gtcacacaggg agtctcggga gatgcgggctg cagcccttca atgagtaccg caagagggtt 1500
160 ggcacgaaac cctacacctc cttccaggag ctctaggag agaaggagat ggcagcagag 1560
162 ttggaggaaat tgtatggaga cattgatgcg ttggagttct accctggact gcttcttgaa 1620
164 aagtgccatc caaactctat ctttggggag agtatgatag agattggggc tcccttttcc 1680
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168 ggcggcgagg tgggctttta cattgtcaag acggccacac tgaagaagct ggtctgcctc 1800
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172 cctgctgtgg agcgaccatc cacagagctc tga 1893
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176 <211> LENGTH: 630
177 <212> TYPE: PRT
178 <213> ORGANISM: Homo sapiens
180 <400> SEQUENCE: 9
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186 Ser Trp Trp Ser Leu Glu Cys Gln Leu Ser Pro Ser Ser Leu Ser Ser
187 20 25 30
190 Ala Gly Ser Leu Leu Leu Trp Phe Leu Leu Phe Leu Leu Leu Leu Pro
191 35 40 45
194 Pro Leu Pro Val Leu Leu Ala Asp Pro Gly Ala Pro Thr Pro Val Asn
195 50 55 60
198 Pro Cys Cys Tyr Tyr Pro Cys Gln His Gln Gly Ile Cys Val Arg Phe
199 65 70 75 80
202 Gly Leu Asp Arg Tyr Gln Cys Asp Cys Thr Arg Thr Gly Tyr Ser Gly
203 85 90 95
206 Pro Asn Cys Thr Ile Pro Gly Leu Trp Thr Trp Leu Arg Asn Ser Leu
207 100 105 110
210 Arg Pro Ser Pro Ser Phe Thr His Phe Leu Leu Thr His Gly Arg Trp
211 115 120 125
214 Phe Trp Glu Phe Val Asn Ala Thr Phe Ile Arg Glu Met Leu Met Arg
215 130 135 140
218 Leu Val Leu Thr Val Arg Ser Asn Leu Ile Pro Ser Pro Pro Thr Tyr
219 145 150 155 160
222 Asn Ser Ala His Asp Tyr Ile Ser Trp Glu Ser Phe Ser Asn Val Ser
223 165 170 175
226 Tyr Tyr Thr Arg Ile Leu Pro Ser Val Pro Lys Asp Cys Pro Thr Pro
227 180 185 190
230 Met Gly Thr Lys Gly Lys Lys Gln Leu Pro Asp Ala Gln Leu Leu Ala
231 195 200 205
234 Arg Arg Phe Leu Leu Arg Arg Lys Phe Ile Pro Asp Pro Gln Gly Thr
235 210 215 220
238 Asn Leu Met Phe Ala Phe Phe Ala Gln His Phe Thr His Gln Phe Phe
239 225 230 235 240
242 Lys Thr Ser Gly Lys Met Gly Pro Gly Phe Thr Lys Ala Leu Gly His
243 245 250 255
246 Gly Val Asp Leu Gly His Ile Tyr Gly Asp Asn Leu Glu Arg Gln Tyr
247 260 265 270
250 Gln Leu Arg Leu Phe Lys Asp Gly Lys Leu Lys Tyr Gln Val Leu Asp
251 275 280 285

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258 Tyr Pro Arg Gly Ile Pro Pro Gln Ser Gln Met Ala Val Gly Gln Glu
259 305                      310                      315                      320
262 Val Phe Gly Leu Leu Pro Gly Leu Met Leu Tyr Ala Thr Leu Trp Leu
263                      325                      330                      335
266 Arg Glu His Asn Arg Val Cys Asp Leu Leu Lys Ala Glu His Pro Thr
267                      340                      345                      350
270 Trp Gly Asp Glu Gln Leu Phe Gln Thr Thr Arg Leu Ile Leu Ile Gly
271                      355                      360                      365
274 Glu Thr Ile Lys Ile Val Ile Glu Glu Tyr Val Gln Gln Leu Ser Gly
275      370                      375                      380
278 Tyr Phe Leu Gln Leu Lys Phe Asp Pro Glu Leu Leu Phe Gly Val Gln
279 385                      390                      395                      400
282 Phe Gln Tyr Arg Asn Arg Ile Ala Met Glu Phe Asn His Leu Tyr His
283                      405                      410                      415
286 Trp His Pro Leu Met Pro Asp Ser Phe Lys Val Gly Ser Gln Glu Tyr
287                      420                      425                      430
290 Ser Tyr Glu Gln Phe Leu Phe Asn Thr Ser Met Leu Val Asp Tyr Gly
291                      435                      440                      445
294 Val Glu Ala Leu Val Asp Ala Phe Ser Arg Gln Ile Ala Gly Arg Ile
295      450                      455                      460
298 Gly Gly Gly Arg Asn Met Asp His His Ile Leu His Val Ala Val Asp
299 465                      470                      475                      480
302 Val Ile Arg Glu Ser Arg Glu Met Arg Leu Gln Pro Phe Asn Glu Tyr
303                      485                      490                      495
306 Arg Lys Arg Phe Gly Met Lys Pro Tyr Thr Ser Phe Gln Glu Leu Val
307      500                      505                      510
310 Gly Glu Lys Glu Met Ala Ala Glu Leu Glu Glu Leu Tyr Gly Asp Ile
311                      515                      520                      525
314 Asp Ala Leu Glu Phe Tyr Pro Gly Leu Leu Leu Glu Lys Cys His Pro
315      530                      535                      540
318 Asn Ser Ile Phe Gly Glu Ser Met Ile Glu Ile Gly Ala Pro Phe Ser
319 545                      550                      555                      560
322 Leu Lys Gly Leu Leu Gly Asn Pro Ile Cys Ser Pro Glu Tyr Trp Lys
323                      565                      570                      575
326 Pro Ser Thr Phe Gly Gly Glu Val Gly Phe Asn Ile Val Lys Thr Ala
327                      580                      585                      590
330 Thr Leu Lys Lys Leu Val Cys Leu Asn Thr Lys Thr Cys Pro Tyr Val
331                      595                      600                      605
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339 625                      630
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343 <211> LENGTH: 1860
344 <212> TYPE: DNA
345 <213> ORGANISM: Homo sapiens
347 <400> SEQUENCE: 10

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352 ttgctgttcc tgctcctgct cccgcgcctc cccgtcctgc tcgcggaccc aggggcgccc      180
354 acgccagtga atccctgttg ttactatcca tgccagcacc agggcatctg tgtccgcttc      240
356 ggccttgacc gctaccagtg tgactgcacc cgcacgggct attccggccc caactgcacc      300
358 atccctggcc tgtggacctg gctccggaat tcaactgcggc ccagcccctc tttcacccac      360
360 ttcttgc tca ctacggggcg ctggttctgg gagtttgtca atgccacctt catccgagag      420
362 atgctcatgc gcttggactt cacagtgcgc tccaacctta tccccagtc cccacactac      480
364 aactcagcac atgactacat cagctgggag tctttctcca acgtgagcta ttacactcgt      540
366 attctgccc t ctgtgcctaa agattgcccc acaccatgg gaaccaaagg gaagaagcag      600
368 ttgccagatg cccagctcct ggcccgcgcg ttcttgc tca ggaggaagtt catacctgac      660
370 ccccaaggca ccaacctcat gtttgccttc tttgcacaac acttcacca ccagttcttc      720
372 aaaacttctg gcaagatggg tcttggtctt accaaggcct tggggccatgg ggtagacctc      780
374 gggccatttt atggagacaa tctggagcgt cagtatcaac tgcggctctt taaggatggg      840
376 aaactcaagt accaggtgct ggatggagaa atgtaccgcg cctcggtaga agaggcgcct      900
378 gtgttgatgc actacccccg aggcattccc cccagagcc agatggctgt gggccaggag      960
380 gtgtttgggc tgcttctctg gctcatgctg tatgccacgc tctggctacg tgagcacaac     1020
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402 aagtgccatc caaactctat ctttggggag agtatgatag agattggggc tcccttttcc     1680
404 ctcaagggtc tcttagggaa tccactctgt tctccggagt actggaagcc gagcacattt     1740
406 ggcggcgagg tggcgtttaa cattgtcaag acggccacac tgaagaagct ggtctgcctc     1800
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411 &lt;210&gt; SEQ ID NO: 11

412 &lt;211&gt; LENGTH: 630

413 &lt;212&gt; TYPE: PRT

414 &lt;213&gt; ORGANISM: Homo sapiens

416 &lt;400&gt; SEQUENCE: 11

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423          20          25          30
426 Ala Gly Ser Leu Leu Leu Trp Phe Leu Leu Phe Leu Leu Leu Leu Pro
427          35          40          45
430 Pro Leu Pro Val Leu Leu Ala Asp Pro Gly Ala Pro Thr Pro Val Asn
431          50          55          60
434 Pro Cys Cys Tyr Tyr Pro Cys Gln His Gln Gly Ile Cys Val Arg Phe
435 65          70          75          80
438 Gly Leu Asp Arg Tyr Gln Cys Asp Cys Thr Arg Thr Gly Tyr Ser Gly
439          85          90          95
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**VERIFICATION SUMMARY**

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